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SEQUENCE LISTING

<110> INSERM

<120> Human  $\beta$ TrCP protein for targeting proteins towards proteasome degradation pathways

<140> PCT/FR99/00196

<141> 1999-01-29

<150> FR98 01100

<151> 1998-01-30

<150> FR98 15545

<151> 1998-12-09

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 2151

<212> ADN

<213> Artificial sequence

<220>

<221> CDS

<222> (70)..(1776)

<220>

<223> Description of the artificial sequence : ADNc  
coding for human  $\beta$ TrCP protein

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tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111  
Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys  
1 5 10

ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159  
Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro  
15 20 25 30

agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207  
Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser  
35 40 45

tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255  
Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr  
50 55 60

gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303  
Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly  
65 70 75

act tcc agt atg att gtg ccc aag caa cgg aaa ctc tca gca agc tat 351  
Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr  
80 85 90

gaa aag gaa aag gaa ctg tgt gtc aaa tac ttt gag cag tgg tca gag 399  
Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu  
95 100 105 110

tca gat caa gtg gaa ttt gtg gaa cat ctt ata tcc caa atg tgt cat		447	
Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His			
115	120	125	
tac caa cat ggg cac ata aac tcg tat ctt aaa cct atg ttg cag aga		495	
Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg			
130	135	140	
gat ttc ata act gct ctg cca gct cgg gga ttg gat cat atc gct gag		543	
Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu			
145	150	155	
aac att ctg tca tac ctg gat gcc aaa tca cta tgt gct gct gaa ctt		591	
Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu			
160	165	170	
gtg tgc aag gaa tgg tac cga gtg acc tct gat ggc atg ctg tgg aag		639	
Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys			
175	180	185	190
aag ctt atc gag aga atg gtc agg aca gat tct ctg tgg aga ggc ctg		687	
Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu			
195	200	205	
gca gaa cga aga gga tgg gga cag tat tta ttc aaa aac aaa cct cct		735	
Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro			
210	215	220	
gac ggg aat gct cct ccc aac tct ttt tat aga gca ctt tat cct aaa		783	
Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys			
225	230	235	
att ata caa gac att gag aca ata gaa tct aat tgg aga tgt gga aga		831	
Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg			
240	245	250	
cat agt tta cag aga att cac tgc cga agt gaa aca agc aaa gga gtt		879	
His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val			
255	260	265	270
tac tgt tta cag tat gat gat cag aaa ata gta agc ggc ctt cga gac		927	
Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp			
275	280	285	
aac aca atc aag atc tgg gat aaa aac aca ttg gaa tgc aag cga att		975	
Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile			
290	295	300	
ctc aca ggc cat aca ggt tca gtc ctc tgt ctc cag tat gat gag aga		1023	
Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg			
305	310	315	
gtg atc ata aca gga tca tcg gat tcc acg gtc aga gtg tgg gat gta		1071	
Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val			
320	325	330	
aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt		1119	
Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val			
335	340	345	350
ctg cac ttg cgt ttc aat aat ggc atg atg gtg acc tgc tcc aaa gat		1167	
Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp			
355	360	365	

cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc 1215  
 Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu  
 370 375 380

cgg agg gtg ctg gtc gga cac cga gct gct gtc aat gtt gta gac ttt 1263  
 Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe  
 385 390 395

gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta 1311  
 Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val  
 400 405 410

tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa 1359  
 Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys  
 415 420 425 430

cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtg agt ggc 1407  
 Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly  
 435 440 445

tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt 1455  
 Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys  
 450 455 460

tta cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt 1503  
 Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe  
 465 470 475

gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtg 1551  
 Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val  
 480 485 490

tgg gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc 1599  
 Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu  
 495 500 505 510

tgt cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag 1647  
 Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln  
 515 520 525

ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc 1695  
 Phe Asp Glu Phe Gln Ile Val Ser Ser His Asp Asp Thr Ile Leu  
 530 535 540

atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt 1743  
 Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg  
 545 550 555

tcc cct tct cga aca tac acc tac atc tcc aga taaaataacca tacactgacc 1796  
 Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg  
 560 565

tcataacttgc ccaggaccca taaaagttgc ggtatataac gtatctgcca ataccaggat 1856  
 gagcaacaac agtaacaatc aaactactgc ccagttccc tggactagcc gaggagcagg 1916

gctttgagac tcctgttggg acacagttgg tctgcagtcg gcccaggacg gtctactcag 1976  
 cacaactgac tgcttcagtg ctgctatcag aagatgtctt ctatcaattg tgaatgattg 2036  
 gaactttaa acctccccctc ctctcctcct ttcacctctg cacctagttt tttcccatgg 2096  
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<210> 2  
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<220>  
 <223> Description of the artificial sequence : ADNc  
 coding for human  $\beta$ TrCP protein

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Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys  
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Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala  
 35 40 45

Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met  
 50 55 60

Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser  
 65 70 75 80

Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys  
 85 90 95

Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp  
 100 105 110

Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln  
 115 120 125

His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe  
 130 135 140

Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile  
 145 150 155 160

Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys  
 165 170 175

Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu  
 180 185 190

Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu  
 195 200 205

Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly  
 210 215 220

Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile  
 225 230 235 240

Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser  
 245 250 255

Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys  
 260 265 270

Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr  
 275 280 285

Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr  
 290 295 300

Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile  
 305 310 315 320  
 Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr  
 325 330 335  
 Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His  
 340 345 350  
 Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser  
 355 360 365  
 Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg  
 370 375 380  
 Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp  
 385 390 395 400  
 Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn  
 405 410 415  
 Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly  
 420 425 430  
 Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser  
 435 440 445  
 Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg  
 450 455 460  
 Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn  
 465 470 475 480  
 Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp  
 485 490 495  
 Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu  
 500 505 510  
 Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp  
 515 520 525  
 Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp  
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 545 550 555 560  
 Ser Arg Thr Tyr Thr Tyr Ile Ser Arg  
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 <213> Artificial sequence

<220>  
 <223> Description of the artificial sequence : sense primer

<400> 3  
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<210> 4  
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 <212> ADN  
 <213> Artificial sequence  
  
 <220>  
 <223> Description of the artificial sequence : antisense primer

<400> 4  
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<210> 5  
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 <212> ADN  
 <213> Artificial sequence  
  
 <220>  
 <223> Description of the artificial sequence : sense primer

<400> 5  
 ggatgatgta tataactatc

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<210> 6  
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 <213> Artificial sequence  
  
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 <223> Description of the artificial sequence : antisense primer

<400> 6  
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 <223> Description of the artificial sequence : primer

<400> 7  
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<210> 8  
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 <212> ADN  
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 <220>  
 <223> Description of the artificial sequence : primer

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